

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5

## (i) APPLICANT:

- (A) NAME: DANISCO A/S
- (B) STREET: Langebrogade 1
- (C) CITY: Copenhagen
- 10 (E) COUNTRY: Denmark
- (F) POSTAL CODE (ZIP): 1001 K
- (G) TELEPHONE: +45 32 66 22 00
- (H) TELEFAX: +45 32 66 21 67

15 15 (ii) TITLE OF INVENTION: Cloning and use of Lipase 3 gene from  
Aspergillus tubigensis

(iii) NUMBER OF SEQUENCES: 9

20 20 (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

25

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

30 30 (A) LENGTH: 25 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 35 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (vi) ORIGINAL SOURCE:

40 40 (A) ORGANISM: Aspergillus tubigensis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Ser Val Ser Thr Ser Thr Leu Asp Glu Leu Gln Leu Phe Ala Gln Trp  
1 5 10 15

5

Ser Ala Ala Ala Tyr Xaa Ser Asn Asn  
20 25

(2) INFORMATION FOR SEQ ID NO: 2:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

20

(v) FRAGMENT TYPE: internal

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Aspergillus tubigensis

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Val His Thr Gly Phe Trp Lys  
1 5

30

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

40

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Aspergillus tubigensis

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ala Trp Glu Ser Ala Ala Asp Glu Leu Thr Ser Lys Ile Lys  
5 1 5 10

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "Oligonucleotide"

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TTCCARAANC CNGTRTGNAC

20

25 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "Oligonucleotide"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

40

CARYTNTTYG CNCARTGG

18

(2) INFORMATION FOR SEQ ID NO: 6:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "Oligonucleotide"

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCVGCHSWYT CCCAVGC

17

15 (2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "PCR fragment"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

30 CAGTTGTTCG CGCAATGGTC TGCCGCAGCT TATTGCTCGA ATAATATCGA CTCGAAAGAV 60

TCCAACATTGA CATGCACGGC CAACGCCTGT CCATCAGTCG AGGAGGCCAG TACCACGATG 120

35 CTGCTGGAGT TCGACCTGTA TGTCACTCAG ATCGCAGACA TAGAGCACAG CTAATTGAAC 180

AGGACGAACG ACTTTGGAG GCACAGCCGG TTTCTGGCC GCGGACAACA CCAACAAGCG 240

GCTCGTGGTC GCCTTCCGGG GAAGCAGCAC GATTGAGAAC TGGATTGCTA ATCYTGACTT 300

40 CATCCTGGRA GATAACG 317

(2) INFORMATION FOR SEQ ID NO: 8:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1045 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus tubigensis*

10 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:join(1..82, 135..300, 347..683, 737..1045)

(ix) FEATURE:

15 (A) NAME/KEY: sig\_peptide

(B) LOCATION:1..81

(ix) FEATURE:

20 (A) NAME/KEY: mat\_peptide

(B) LOCATION:join(82, 135..300, 347..683, 737..1042)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

25 ATG TTC TCT GGA CGG TTT GGA GTG CTT TTG ACA GCG CTT GCT GCG CTG 48  
 Met Phe Ser Gly Arg Phe Gly Val Leu Leu Thr Ala Leu Ala Ala Leu  
 -27 -25 -20 -15

GGT GCT GCC GCG CCG GCA CCG CTT GCT GTG CGG A GTAGGTGTGC 92  
 30 Gly Ala Ala Ala Pro Ala Pro Leu Ala Val Arg  
 -10 -5

CCGATGTGAG ATGGTTGGAT AGCACTGATG AAGGGTGAAT AG GT GTC TCG ACT 145  
 Ser Val Ser Thr  
 35 1

TCC ACG TTG GAT GAG TTG CAA TTG TTC GCG CAA TGG TCT GCC GCA GCT 193  
 Ser Thr Leu Asp Glu Leu Gln Leu Phe Ala Gln Trp Ser Ala Ala Ala  
 5 10 15 20

40 TAT TGC TCG AAT AAT ATC GAC TCG AAA GAC TCC AAC TTG ACA TGC ACG 241  
 Tyr Cys Ser Asn Asn Ile Asp Ser Lys Asp Ser Asn Leu Thr Cys Thr  
 25 30 35

45 GCC AAC GCC TGT CCA TCA GTC GAG GAG GCC AGT ACC ACG ATG CTG CTG 289  
 Ala Asn Ala Cys Pro Ser Val Glu Glu Ala Ser Thr Thr Met Leu Leu

	40	45	50	
	GAG TTC GAC CT GTATGTCACT CAGATCGCAG ACATAGAGCA CAGCTAATTT			340
	Glu Phe Asp Leu			
5	55			
	GAACAG G ACG AAC GAC TTT GGA GGC ACA GCC GGT TTC CTG GCC GCG GAC			389
	Thr Asn Asp Phe Gly Gly Thr Ala Gly Phe Leu Ala Ala Asp			
	60	65	70	
10				
	AAC ACC AAC AAG CGG CTC GTG GTC GCC TTC CGG GGA AGC AGC ACG ATT			437
	Asn Thr Asn Lys Arg Leu Val Val Ala Phe Arg Gly Ser Ser Thr Ile			
	75	80	85	
15	GAG AAC TGG ATT GCT AAT CTT GAC TTC ATC CTG GAA GAT AAC GAC GAC			485
	Glu Asn Trp Ile Ala Asn Leu Asp Phe Ile Leu Glu Asp Asn Asp Asp			
	90	95	100	
20	CTC TGC ACC GGC TGC AAG GTC CAT ACT GGT TTC TGG AAG GCA TGG GAG			533
	Leu Cys Thr Gly Cys Lys Val His Thr Gly Phe Trp Lys Ala Trp Glu			
	105	110	115	
	TCC GCT GCC GAC GAA CTG ACG AGC AAG ATC AAG TCT GCG ATG AGC ACG			581
	Ser Ala Ala Asp Glu Leu Thr Ser Lys Ile Lys Ser Ala Met Ser Thr			
25	120	125	130	
	TAT TCG GGC TAT ACC CTA TAC TTC ACC GGG CAC AGT TTG GGC GGC GCA			629
	Tyr Ser Gly Tyr Thr Leu Tyr Phe Thr Gly His Ser Leu Gly Gly Ala			
	135	140	145	150
30				
	TTG GCT ACG CTG GGA GCG ACA GTT CTG CGA AAT GAC GGA TAT AGC GTT			677
	Leu Ala Thr Leu Gly Ala Thr Val Leu Arg Asn Asp Gly Tyr Ser Val			
	155	160	165	
35	GAG CTG GTGAGTCCTT CACAAAGGTG ATGGAGCGAC AATCGGGAAC AGACAGTC			733
	Glu Leu			
	TAG TAC ACC TAT GGA TGT CCT CGA ATC GGA AAC TAT GCG CTG GCT GAG			781
40	Tyr Thr Tyr Gly Cys Pro Arg Ile Gly Asn Tyr Ala Leu Ala Glu			
	170	175	180	
	CAT ATC ACC AGT CAG GGA TCT GGG GCC AAC TTC CGT GTT ACA CAC TTG			829
	His Ile Thr Ser Gln Gly Ser Gly Ala Asn Phe Arg Val Thr His Leu			
45	185	190	195	

AAC GAC ATC GTC CCC CGG GTG CCA CCC ATG GAC TTT GGA TTC AGT CAG	877
Asn Asp Ile Val Pro Arg Val Pro Pro Met Asp Phe Gly Phe Ser Gln	
5 200 205 210 215	
CCA AGT CCG GAA TAC TGG ATC ACC AGT GGC AAT GGA GCC AGT GTC ACG	925
Pro Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asn Gly Ala Ser Val Thr	
220 225 230	
10 GCG TCG GAT ATC GAA GTC ATC GAG GGA ATC AAT TCA ACG GCG GGA AAT	973
Ala Ser Asp Ile Glu Val Ile Glu Gly Ile Asn Ser Thr Ala Gly Asn	
235 240 245	
15 GCA GGC GAA GCA ACG GTG AGC GTT GTG GCT CAC TTG TGG TAC TTT TTT	1021
Ala Gly Glu Ala Thr Val Ser Val Val Ala His Leu Trp Tyr Phe Phe	
250 255 260	
GCG ATT TCC GAG TGC CTG CTA TAA	1045
20 Ala Ile Ser Glu Cys Leu Leu *	
265 270	

## (2) INFORMATION FOR SEQ ID NO: 9:

25

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

30

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Phe Ser Gly Arg Phe Gly Val Leu Leu Thr Ala Leu Ala Ala Leu	
35 -27 -25 -20 -15	

Gly Ala Ala Ala Pro Ala Pro Leu Ala Val Arg Ser Val Ser Thr Ser	
-10 -5 1 5	

40 Thr Leu Asp Glu Leu Gln Leu Phe Ala Gln Trp Ser Ala Ala Ala Tyr	
10 15 20	

Cys Ser Asn Asn Ile Asp Ser Lys Asp Ser Asn Leu Thr Cys Thr Ala	
25 30 35	

45

Asn Ala Cys Pro Ser Val Glu Glu Ala Ser Thr Thr Met Leu Leu Glu	
---	--

	40	45	50
	Phe Asp Leu Thr Asn Asp Phe Gly Gly Thr Ala Gly Phe Leu Ala Ala		
55	60	65	
5			
	Asp Asn Thr Asn Lys Arg Leu Val Val Ala Phe Arg Gly Ser Ser Thr		
70	75	80	85
	Ile Glu Asn Trp Ile Ala Asn Leu Asp Phe Ile Leu Glu Asp Asn Asp		
10	90	95	100
	Asp Leu Cys Thr Gly Cys Lys Val His Thr Gly Phe Trp Lys Ala Trp		
	105	110	115
15	Glu Ser Ala Ala Asp Glu Leu Thr Ser Lys Ile Lys Ser Ala Met Ser		
	120	125	130
	Thr Tyr Ser Gly Tyr Thr Leu Tyr Phe Thr Gly His Ser Leu Gly Gly		
	135	140	145
20			
	Ala Leu Ala Thr Leu Gly Ala Thr Val Leu Arg Asn Asp Gly Tyr Ser		
	150	155	160
			165
	Val Glu Leu Tyr Thr Tyr Gly Cys Pro Arg Ile Gly Asn Tyr Ala Leu		
25	170	175	180
	Ala Glu His Ile Thr Ser Gln Gly Ser Gly Ala Asn Phe Arg Val Thr		
	185	190	195
30	His Leu Asn Asp Ile Val Pro Arg Val Pro Pro Met Asp Phe Gly Phe		
	200	205	210
	Ser Gln Pro Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asn Gly Ala Ser		
	215	220	225
35			
	Val Thr Ala Ser Asp Ile Glu Val Ile Glu Gly Ile Asn Ser Thr Ala		
	230	235	240
			245
	Gly Asn Ala Gly Glu Ala Thr Val Ser Val Val Ala His Leu Trp Tyr		
40	250	255	260
	Phe Phe Ala Ile Ser Glu Cys Leu Leu *		
	265	270	